

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: September 28, 2004, 09:00:23 / Search time 16.2 Seconds
(without alignments)
57.362 Million cell updates/sec

Title: US-10-084-813-13

Sequence: 1 SOYGFNPNFQIKYVIG 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents, AA.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	96	100.0	54	4	US-08-833-752-11
2	96	100.0	352	3	US-08-466-341D-2
3	96	100.0	352	3	US-09-087-232A-13
4	96	100.0	352	3	US-08-861-105-14
5	96	100.0	352	3	US-08-575-967A-2
6	96	100.0	352	3	US-09-045-583-52
7	96	100.0	352	4	US-09-517-602-5
8	96	100.0	352	4	US-09-534-185-52
9	96	100.0	352	4	US-08-833-752-5
10	96	100.0	352	4	US-09-502-783A-2
11	96	100.0	352	4	US-09-796-202-1
12	82	85.4	21	3	US-08-907-468-11
13	74	77.1	354	4	US-08-724-984A-2
14	47	49.0	355	4	US-09-886-319A-13
15	45	46.9	355	4	US-09-045-583-53
16	45	46.9	355	4	US-09-534-185-53
17	43.5	45.3	352	4	US-09-489-039A-13500
18	43	44.8	172	4	US-09-621-976-4131
19	43	44.8	344	3	US-08-681-192-2
20	42	43.8	460	3	US-08-935-263-4
21	42	43.8	460	3	US-09-594-183-4
22	41	42.7	160	4	US-09-540-236-3023
23	41	42.7	160	4	US-09-328-352-6593
24	41	42.7	255	4	US-09-491-577-2
25	41	42.7	255	4	US-09-252-991A-25052
26	40	41.7	254	4	US-09-134-001C-4582
27	40	41.7	311	4	US-09-134-001C-5171

28	40	41.7	316	4	US-09-489-039A-8904	Sequence 8904, Ap
29	40	41.7	355	1	US-08-012-988A-2	Sequence 2, Appl
30	40	41.7	355	3	US-08-450-393A-5	Sequence 5, Appl
31	40	41.7	355	3	US-08-446-669-5	Sequence 5, Appl
32	40	41.7	355	4	US-09-239-938-1	Sequence 1, Appl
33	40	41.7	355	4	US-08-833-752-9	Sequence 9, Appl
34	40	41.7	355	4	US-09-886-319A-14	Sequence 14, Appl
35	40	41.7	355	5	PCT-0595-00476-5	Sequence 5, Appl
36	40	41.7	371	3	US-08/622	INFORMATION FOR
37	40	41.7	371	4	US-09-165-922A-10	Sequence 10, Appl
38	40	41.7	659	4	US-08-252-991A-26013	Sequence 26013, A
39	40	41.7	2037	4	US-09-543-681A-5538	Sequence 5538, Ap
40	40	40.6	92	4	US-09-328-352-5171	Sequence 5171, Ap
41	40	40.6	448	4	US-09-134-000C-3794	Sequence 3794, Ap
42	39	40.6	452	4	US-09-530-836-6	Sequence 6, Appl
43	39	40.6	485	4	US-09-134-000C-6031	Sequence 6031, Ap
44	39	40.6	598	2	US-08-853-659A-53	Sequence 53, Appl
45	39	40.6	664	4	US-09-377-497-70	Sequence 70, Appl

ALIGNMENTS

RESULT 1
US-08-833-752-11
Sequence 11, Application US/08833752
Patent No. 6448375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASBART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Krobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-833-752-11
Query Match: 100.0%; Score 96; DB 4; Length 54;
Best Local Similarity: 100.0%; Pred. No. 5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOYGFNPNFQIKYVIG 18
DB 9 SOYGFNPNFQIKYVIG 26
RESULT 2

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OM protein - protein search, using nw model

Run on: September 28, 2004, 08:51:21; Search time 52.525 seconds

(without alignment)
118,345 Million cell updates/sec

Title: US-10-084-813-12

Sequence: 1 QMDFGNTMCGLTGTYFGFSS 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: A_Geneseq_293and04

1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	126	100.0	22	4 AAB88994	AAB88994 HIV gp120
2	126	100.0	184	4 AAB88994	AAB88994 HIV gp120
3	126	100.0	215	2 AAB88994	AAB88994 HIV gp120
4	126	100.0	215	2 AAB88994	AAB88994 HIV gp120
5	126	100.0	268	7 ADC10144	ADC10144 Human NOV
6	126	100.0	332	2 AAB88994	AAB88994 HIV gp120
7	126	100.0	332	2 AAB88994	AAB88994 HIV gp120
8	126	100.0	352	2 AAB88994	AAB88994 HIV gp120
9	126	100.0	352	2 AAB88994	AAB88994 HIV gp120
10	126	100.0	352	2 AAB88994	AAB88994 HIV gp120
11	126	100.0	352	2 AAB88994	AAB88994 HIV gp120
12	126	100.0	352	2 AAB88994	AAB88994 HIV gp120
13	126	100.0	352	2 AAB88994	AAB88994 HIV gp120
14	126	100.0	352	2 AAB88994	AAB88994 HIV gp120
15	126	100.0	352	2 AAB88994	AAB88994 HIV gp120
16	126	100.0	352	2 AAB88994	AAB88994 HIV gp120
17	126	100.0	352	2 AAB88994	AAB88994 HIV gp120
18	126	100.0	352	2 AAB88994	AAB88994 HIV gp120
19	126	100.0	352	2 AAB88994	AAB88994 HIV gp120
20	126	100.0	352	2 AAB88994	AAB88994 HIV gp120
21	126	100.0	352	2 AAB88994	AAB88994 HIV gp120
22	126	100.0	352	2 AAB88994	AAB88994 HIV gp120
23	126	100.0	352	2 AAB88994	AAB88994 HIV gp120
24	126	100.0	352	2 AAB88994	AAB88994 HIV gp120
25	126	100.0	352	2 AAB88994	AAB88994 HIV gp120

26	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
27	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
28	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
29	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
30	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
31	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
32	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
33	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
34	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
35	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
36	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
37	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
38	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
39	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
40	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
41	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
42	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
43	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
44	126	100.0	352	5 AAB88994	AAB88994 HIV gp120
45	126	100.0	371	2 AAB88994	AAB88994 HIV gp120

ALIGNMENTS

RESULT 1	AAB88994	AAB88994 standard, peptide, 22 AA.
XX	22-MAY-2001 (first entry)	
XX	HIV gp120 protein binding peptide #87.	
XX	Human chemokine receptor, CD4, HIV, glycoprotein 120, gp120; antagonist;	
XX	replication, CCR5, CCR4, CD4, STRL3.	
XX	Homo sapiens.	
XX	WO200116182-A2.	
XX	08-MAR-2001.	
XX	25-MAR-2001; 2000MO-US023505.	
XX	27-MAR-1999; 99US-0151270P.	
XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
XX	Saxinger C;	
XX	WPI: 2001-244398/25.	
XX	Novel polypeptides useful for treating HIV infection, have homology to	
XX	PT regions of domain of human chemokine receptors CCR5, CCR4 and STRL3,	
XX	and bind to HIV gp120 under physiological conditions.	
XX	Claim 21, Page 38, 114pp; English.	
XX	The present invention describes a number of peptides which are able to	
XX	bind to HIV glycoprotein 120 (gp120). These are similar to the human	
XX	chemokine receptors CCR5, CCR4 and STRL3, as well as CD4. These are	
XX	useful in the treatment of HIV, as they prevent replication of the virus.	
XX	The present sequence is an example of a peptide of the invention	
XX	Sequence 22 AA:	
XX	Query Match 100.0%; Score 126; DB 4; Length 22;	
XX	Best Local Similarity 100.0%; Pred. No. 1.2e-12;	
XX	Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX	1 QMDFGNTMCGLTGTYFGFSS 22	

DB 1 QMDPNTMCOILLTGILYPIGFPS 22

RESULT 2

ID AAW27406 standard; protein, 184 AA.

XX AAW27406;

DT 14-APR-1998 (first entry)

DB Inactive human CCR5.

XX Inactive; human Cys-Cys chemokine receptor-5; CCR5;

XX human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;

XX predisposition; resistance; diagnosis; treatment; prevention;

XX inflammatory diseases; rheumatoid arthritis; glomerulonephritis; asthma;

XX idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;

XX atherosclerosis; autoimmune disorder.

XX Homo sapiens.

XX W09732019-A2.

XX 04-SEP-1997.

XX 28-FEB-1997; 97NC-BE000023.

XX 01-MAR-1996; 96EP-00870021.

XX 06-AUG-1996; 96EP-00870102.

XX (EURO-) EUROSCREEN SA.

XX Samson M, Parmentier M, Vassart G, Libert F,

XX WPI; 1997-479829/44.

XX N-PSDB; AAT90116.

XX Active and inactive forms of human CC chemokine receptor CCR-5 - useful

XX to diagnose, prevent and/or treat inflammatory disorders, autoimmune

XX disease and viral infection.

XX Claim 1; Fig 1a; 94pp; English.

XX The present sequence is an inactive human CC (Cys-Cys) chemokine receptor

XX 5 (CCR5), which is not a receptor of human immunodeficiency virus type 1

XX or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to diagnose, treat

XX and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,

XX glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,

XX viral infections, especially HIV-1 or HIV-2 infection, cancer,

XX atherosclerosis and autoimmune disorders. Subjects that express the

XX inactive receptor have a predisposition, or resistance to HIV-1 and/or

XX HIV-2

XX Sequence 184 AA;

XX Query Match 100.0%; Score 126; DB 2; Length 184;

XX Best Local Similarity 100.0%; Pred. No. 1, 2e-11;

XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE Inactive human CCR5.

XX Inactive; human Cys-Cys chemokine receptor 5; CCR5;

XX human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;

XX predisposition; resistance; diagnosis; treatment; prevention;

XX inflammatory diseases; rheumatoid arthritis; glomerulonephritis; asthma;

XX idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;

XX atherosclerosis; autoimmune disorder.

XX Homo sapiens.

XX W09732019-A2.

XX 04-SEP-1997.

XX 28-FEB-1997; 97NC-BE000023.

XX 01-MAR-1996; 96EP-00870021.

XX 06-AUG-1996; 96EP-00870102.

XX (EURO-) EUROSCREEN SA.

XX Samson M, Parmentier M, Vassart G, Libert F;

XX WPI; 1997-479829/44.

XX N-PSDB; AAT90116.

XX Active and inactive forms of human CC chemokine receptor CCR-5 - useful

XX to diagnose, prevent and/or treat inflammatory disorders, autoimmune

XX disease and viral infection.

XX Claim 7; Fig 1d-e; 94pp; English.

XX The present sequence is an inactive human CC (Cys-Cys) chemokine receptor

XX 5 (CCR5), which lacks the last 3 transmembrane regions and the regions

XX involved in G protein-coupling. CCR5 or its cDNA can be used to diagnose,

XX treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,

XX glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,

XX viral infections, especially human immunodeficiency virus type 1 or type

XX 2 (HIV-1 or HIV-2) infection, cancer, atherosclerosis and autoimmune

XX disorders. Subjects that express the inactive receptor have a

XX predisposition, or resistance to HIV-1 and/or HIV-2

XX Sequence 215 AA;

XX Query Match 100.0%; Score 126; DB 2; Length 215;

XX Best Local Similarity 100.0%; Pred. No. 1, 5e-11;

XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 QMDPNTMCOILLTGILYPIGFPS 22

DB 93 QMDPNTMCOILLTGILYPIGFPS 114

RESULT 4

ID AAW88238 standard; protein, 215 AA.

XX AAW88238;

XX 15-MAR-1999 (first entry).

DB HIV-1 co-receptor CCR5 variant CCR5-delta32.

XX HIV-1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS;

XX gene therapy; human.

XX Homo sapiens.

XX Key

XX Domain

XX Location/Qualifiers

XX 32..56

XX /note="transmembrane domain 1"

Tue Sep 28 15:49:55 2004

us-10-084-813-12.ra1

Page 2

US-09-087-232A-17

Sequence 17, Application US/09087232A

Patent No. 6154311

GENERAL INFORMATION:

APPLICANT: Quilient et al.

TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR

TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESS: Baker & Bottj, L.L.P. attn. Lisa Kule

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/087.232A

FILING DATE: 28 MAY 1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/048,057

FILING DATE: 30 MAY 1997

ATTORNEY/AGENT INFORMATION:

NAME: KOLE, LISA B.

REGISTRATION NUMBER: 35,225

REFERENCE/DOCKET NUMBER: AP 31115

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 408-2628

TELEFAX: (212) 765-2519

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-087-232A-17

Query Match

Best Local Similarity 100.0%

Matches 22: Conservative 0, Mismatches 0, Indels 0, Gaps 0

DB 1 QMDPNTMCOLLTLTYPTGPGS 22

93 QMDPNTMCOLLTLTYPTGPGS 114

US-08-833-752-6

Sequence 6, Application US/0883752

Patent No. 6448375

GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL

APPLICANT: PARENTIER, MARC

APPLICANT: VASSART, GILBERT

APPLICANT: LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESS: Knoppe, Martens, Olson & Bear

STREET: 610 Newport Center Drive 16th floor

CITY: Newport Beach

STATE: CA

COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/833,752

FILING DATE: 9-APR-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-833-752-6

Query Match

Best Local Similarity 100.0%

Matches 22: Conservative 0, Mismatches 0, Indels 0, Gaps 0

DB 1 QMDPNTMCOLLTLTYPTGPGS 22

93 QMDPNTMCOLLTLTYPTGPGS 114

US-08-466-343D-2

Sequence 2, Application US/08466343D

Patent No. 6025154

GENERAL INFORMATION:

APPLICANT: LI, YI

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN

TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGMR10 (AS AMENDED)

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., NW, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,343D

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488,1150000/EKS/KLM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-466-343D-2

Query Match

Best Local Similarity 100.0%

Matches 22: Conservative 0, Mismatches 0, Indels 0, Gaps 0

DB 1 QMDPNTMCOLLTLTYPTGPGS 22

93 QMDPNTMCOLLTLTYPTGPGS 114

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OM protein - protein search, using sw model

Run on: September 28, 2004, 09:00:23 / Search time 19.8 seconds
(without alignments)

57.362 Million cell updates/sec

Title: US-10-084-813-12

Sequence: 1 QMDPGNTMQLTGLYFIFGFS 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

389414

ALIGNMENTS

28	83	65.9	269	3	US-09-239-268-30	Sequence 30, Appl
29	82	65.1	355	1	US-08-461-244-2	Sequence 2, Appl
30	82	65.1	355	3	US-09-045-583-56	Sequence 56, Appl
31	82	65.1	355	4	US-09-534-185-56	Sequence 56, Appl
32	81	64.3	360	3	US-09-045-583-51	Sequence 51, Appl
33	81	64.3	360	4	US-09-534-185-51	Sequence 51, Appl
34	80	63.5	354	4	US-08-724-984-2	Sequence 2, Appl
35	76	60.3	355	4	US-09-886-319A-13	Sequence 13, Appl
36	74	58.7	329	4	US-08-013-988A-2	Sequence 2, Appl
37	71	56.3	355	1	US-08-450-669-5	Sequence 5, Appl
38	71	56.3	355	3	US-09-045-583-53	Sequence 53, Appl
39	71	56.3	355	3	US-09-239-268-1	Sequence 1, Appl
40	71	56.3	355	4	US-09-534-185-53	Sequence 53, Appl
41	71	56.3	355	4	US-09-886-319A-14	Sequence 14, Appl
42	71	56.3	355	5	PCT-US95-00476-5	Sequence 5, Appl
43	71	56.3	355	5	PCT-US95-00476-5	Sequence 5, Appl
44	71	56.3	355	5	PCT-US95-00476-5	Sequence 5, Appl
45	69	54.8	355	4	US-08-833-752-9	Sequence 9, Appl

Total number of hits satisfying chosen parameters: 389414
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: /cgm2_6/prodata/2/1aa/5A_COMB.pdb:
2: /cgm2_6/prodata/2/1aa/5B_COMB.pdb:
3: /cgm2_6/prodata/2/1aa/6A_COMB.pdb:
4: /cgm2_6/prodata/2/1aa/6B_COMB.pdb:
5: /cgm2_6/prodata/2/1aa/PCITUS_COMB.pdb:
6: /cgm2_6/prodata/2/1aa/backfillseq1.pdb:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	126	100.0	184	4	US-08-833-752-4
2	126	100.0	215	3	US-09-087-232A-17
3	126	100.0	215	4	US-08-833-752-6
4	126	100.0	352	3	US-08-466-343D-2
5	126	100.0	352	3	US-09-087-232A-13
6	126	100.0	352	3	US-08-861-102-14
7	126	100.0	352	3	US-08-575-867A-2
8	126	100.0	352	4	US-09-045-583-52
9	126	100.0	352	4	US-09-517-605-5
10	126	100.0	352	4	US-09-534-185-52
11	126	100.0	352	4	US-08-833-752-5
12	126	100.0	352	4	US-09-502-783A-2
13	126	100.0	352	4	US-09-796-202-1
14	87	69.0	344	3	US-08-466-343D-9
15	87	69.0	347	1	US-08-461-244-3
16	87	69.0	360	1	US-08-450-669-4
17	87	69.0	360	3	US-08-446-669-4
18	87	69.0	360	3	US-09-045-583-50
19	87	69.0	360	4	US-09-534-185-50
20	87	69.0	360	4	US-08-833-752-7
21	87	69.0	360	4	US-09-131-827A-2
22	87	69.0	360	4	US-09-131-827A-20
23	87	69.0	374	1	PCT-US95-00476-4
24	87	69.0	374	1	US-08-450-669-2
25	87	69.0	374	2	US-08-446-669-2
26	87	69.0	374	2	PCT-US95-00476-2
27	83	63.9	269	1	US-08-307-499-30

RESULT 1
US-08-833-752-4
Sequence 4, Application US/08833752
Patent No. 6448375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSER: Knobb, Martens, Oleson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel B
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-752-4
Query Match 100.0% Score 126, DB 4, Length 184;
Best Local Similarity 100.0% Pred. No. 1.3e-11;
Matches 22, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
DB 93 QMDPGNTMQLTGLYFIFGFS 114
CY 1 QMDPGNTMQLTGLYFIFGFS 22

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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:51:21 / Search time 42.975 Seconds
(without alignments)
118.345 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95

Sequence: 1 YAFVGEKRNLYLVFQK 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282347505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_29Jan04:*
1: geneseq21980a:*
2: geneseq21990a:*
3: geneseq22000a:*
4: geneseq22010a:*
5: geneseq22020a:*
6: geneseq22030a:*
7: geneseq22040a:*
8: geneseq22050a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	18	4	AA88982 HIV gp120
2	95	100.0	18	4	AA88982 HIV gp120
3	95	100.0	27	5	AA814757 Human CCR
4	95	100.0	43	5	AA814756 Human CCR
5	95	100.0	58	5	AA814755 Human CCR
6	95	100.0	268	7	ADCI0142 Human NOV
7	95	100.0	268	7	ADCI0144 Human NOV
8	95	100.0	332	2	AAW26766 Human che
9	95	100.0	332	2	AAW27407 Human che
10	95	100.0	352	2	AAW27123 Human che
11	95	100.0	352	2	AAW27125 Human che
12	95	100.0	352	2	AAW27125 Human che
13	95	100.0	352	2	AAW27125 Human che
14	95	100.0	352	2	AAW27125 Human che
15	95	100.0	352	2	AAW27125 Human che
16	95	100.0	352	2	AAW27125 Human che
17	95	100.0	352	2	AAW27125 Human che
18	95	100.0	352	2	AAW27125 Human che
19	95	100.0	352	2	AAW27125 Human che
20	95	100.0	352	2	AAW27125 Human che
21	95	100.0	352	2	AAW27125 Human che
22	95	100.0	352	2	AAW27125 Human che
23	95	100.0	352	2	AAW27125 Human che
24	95	100.0	352	2	AAW27125 Human che
25	95	100.0	352	2	AAW27125 Human che

26	95	100.0	352	4	AA883354 Human CCR
27	95	100.0	352	4	AA882948 Human HIV
28	95	100.0	352	4	AAU97150 Human G-P
29	95	100.0	352	5	AAU97152 Human G-P
30	95	100.0	352	5	AAU97152 Human G-P
31	95	100.0	352	5	AAU97152 Human G-P
32	95	100.0	352	5	AAU97152 Human G-P
33	95	100.0	352	5	AAU97152 Human G-P
34	95	100.0	352	5	AAU97152 Human G-P
35	95	100.0	352	5	AAU97152 Human G-P
36	95	100.0	352	5	AAU97152 Human G-P
37	95	100.0	352	5	AAU97152 Human G-P
38	95	100.0	352	5	AAU97152 Human G-P
39	95	100.0	352	5	AAU97152 Human G-P
40	95	100.0	352	5	AAU97152 Human G-P
41	95	100.0	352	5	AAU97152 Human G-P
42	95	100.0	352	5	AAU97152 Human G-P
43	95	100.0	352	5	AAU97152 Human G-P
44	95	100.0	352	5	AAU97152 Human G-P
45	95	100.0	352	5	AAU97152 Human G-P

ALIGNMENTS

RESULT 1	AA88982	standard; peptide; 18 AA.
ID	AA88982	standard; peptide; 18 AA.
AC	AA88982	
DT	23-MAY-2001	(first entry)
DE	HIV gp120 protein binding peptide #75.	
XX	Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;	
XX	replication; CCR5; CXCR4; CD4; STRL33.	
XX	Homo sapiens.	
XX	WO200116182-A2.	
XX	08-MAR-2001.	
XX	25-ADG-2000/ 2000MO-08023505.	
XX	27-ADG-1999/ 99US-0151270P.	
XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
XX	Saxinger C/	
XX	WPI/ 2001-244398/25.	
XX	Novel polypeptides useful for treating HIV infection, have homology to	
XX	regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,	
XX	and binds to HIV gp120 under physiological conditions.	
XX	Example 1; Page 37; 114pp; English.	
XX	The present invention describes a number of peptides which are able to	
XX	bind to HIV glycoprotein 120 (gp120). These are similar to the human	
XX	chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are	
XX	useful in the treatment of HIV, as they prevent replication of the virus.	
XX	The present sequence is an example of a peptide of the invention	
XX	Sequence 18 AA/	
XX	Query Match 100.0%; Score 95; DB 4; Length 18;	
XX	Best Local Similarity 100.0%; Pred. No. 8e-09;	
XX	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX	1 YAFVGEKRNLYLVFQK 18	